

Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims

1. (currently amended) A method for determining the extent of degradation, expressed in terms of a quality value, of ~~a biomolecule~~ an RNA sample, the method comprising:
 - separating the ~~biomolecule~~ RNA sample by ~~one or more molecular characteristics~~ mobility, using an electrophoresis device, to generate ~~measured data~~ an electropherogram,
 - extracting a number of prescribed features from the ~~measured data~~ electropherogram using data analysis, and
 - determining the quality value, which indicates the extent of degradation of the ~~biomolecule~~ RNA sample, from the extracted features using a quality algorithm,wherein the quality algorithm has been derived from:
 - collecting a statistically significant number of trial ~~measured data~~ electropherograms covering a prescribed set of ~~biomolecule~~ RNA samples,
 - assigning a quality label, which indicates the extent that the trial ~~measured data~~ electropherogram exhibits signs of degradation, to every trial ~~measured data~~ electropherogram,
 - extracting features from the trial ~~measured data~~ electropherograms using data analysis,
 - determining functional interrelations among the quality labels and one or more combinations of the extracted features,
 - assigning a rating factor to every functional interrelation, and

specifying the functional interrelation that has the highest rating factor as the quality algorithm.

2. (currently amended) The method of claim 1, further comprising:
 - specifying one or more anomalous cases from among a prescribed number of potentially anomalous cases,
 - extracting a number of prescribed features from the ~~measured data~~ electropherogram of the ~~biomolecule~~ RNA sample using data analysis for every anomalous case,
 - analyzing the ~~measured data~~ electropherogram using an associated anomalous-case algorithm in order to validate every anomalous case identified, and
 - determining the magnitude of the anomaly involved from a combination of the anomalous cases present in order to determine the degree to which the ~~biomolecule~~ RNA sample is anomalous.
3. (previously presented) The method of claim 1, wherein the functional interrelations among the quality labels and the various combinations of extracted features are determined using an adaptive approach.
4. (currently amended) The method of claim 2, wherein the following is carried out in order to determine the anomalous-case algorithm for a prescribed anomalous case:
 - collecting a statistically significant number of trial ~~measured data~~ electropherograms covering a prescribed set of ~~biomolecule~~ RNA samples,
 - assigning an anomalous-case label, which indicates the magnitude of anomaly, to the prescribed anomalous case of every trial ~~measured data~~ electropherogram,

extracting features from the trial ~~measured data~~ electropherogram using data analysis,

determining functional interrelations among the anomalous-case labels and one or more combinations of the extracted features,

assigning a rating factor to every functional interrelation, and

specifying the function interrelation that has the highest rating factor as the anomalous-case algorithm.

5. (previously presented) The method of claim 4, wherein the functional interrelations among the anomalous-case labels and the various combinations of extracted features are determined using an adaptive approach.
6. (original) The method of claim 1, wherein discrete classes are established for the accessible range of measured data quality and every class is assigned a quality label.
7. (previously presented) The method of claim 6, wherein seven classes are established for the quality label.
8. (original) The method of claim 4, wherein 0 and 1 are prescribed as allowed values of the anomalous-case label.
9. (currently amended) The method of claim 1, wherein the ~~measured data are~~ electropherogram is first subdivided into segments in order to before extracting features therefrom.

10. (currently amended) The method of claim 9, wherein ~~the biomolecule sample is an RNA sample, and~~ the following eight regions of the ~~measured data~~ electropherogram of the RNA sample are established as the segments: a preregion, a marker region, a 5S-region, a fast region, an 18S-region, an interregion, a 28S-region, and a postregion.
11. (currently amended) The method of claim 1, wherein positions, heights, and widths of peaks occurring in the ~~measured data~~ electropherogram are determined and their areas computed by integration under the data analysis performed on the ~~measured data~~ electropherogram.
12. (currently amended) The method of claim 9, wherein the ~~measured data~~ electropherogram can be represented as a data curve or a smoothed data curve and wherein one or more of the following prescribed features of the segments of the data curve, or the smoothed data curve, of the ~~measured data~~ electropherogram are determined in the data analysis of the ~~measured data~~ electropherogram:
 - the maximum and minimum value occurring within the segment,
 - the slope and y-intercept of the interpolating straight line fitted to the points on the curve falling within the bounds of the segment,
 - the y-values of this interpolating straight line at the start and end points of the segment,
 - the area under the curve,
 - the area under the interpolating straight line, the ratios of the latter areas to the area under the entire data curve,
 - the deviation of the interpolating straight line from the data curve, or
 - the deviations of the original and smoothed data curve from one another.

13. (previously presented) The method of claim 12, wherein Savitzky-Golay filters and/or the rolling-ball algorithm are employed for smoothing the data curve.
14. (currently amended) The method of claim 10, wherein ~~the biomolecule sample is an RNA sample, and~~ one or more of the following prescribed features are determined in the data analysis of the ~~measured data~~ electropherogram:
 - the ratio of the areas of the 18S-region segment and 28S-region segment to the total area enclosed within the eight segments,
 - the ratio of the area of the 18S-region segment to the area of the 28S-region segment, or
 - the signal/noise ratio.
15. (previously presented) The method of claim 4, wherein the extracted features are consecutively arranged in a list such that the information on the quality label and/or the anomalous-case label will be progressively maximized as each additional feature is added, where each addition of a feature to the list defines a new combination of features.
16. (previously presented) The method of claim 15, wherein the arrangement of extracted features in the list is based on mutual information.
17. (original) The method of claim 3, wherein a neural network is employed as the adaptive approach.
18. (previously presented) The method of claim 17, wherein a Bayesian method is applied for adjusting parameters for the neural network.

19. (original) The method of claim 17, wherein functional interrelations of varying complexity are determined, where the necessary complexity of the functional interrelations sought is obtained by iterative additions of hidden neurons to the neuronal network.
20. (previously presented) The method of claim 18, wherein the a-posteriori probability of the neuronal network computed using a Bayesian method is employed as the rating factor.
- 21-24. (canceled)
25. (currently amended) A non-transitory computer-readable data carrier, for executing or controlling a method for determining the extent of degradation, expressed in terms of a quality value, of ~~a biomolecule~~ an RNA sample based on ~~measured data~~ an electropherogram of the ~~biomolecule~~ RNA sample, the method comprising:
- extracting a number of prescribed features from the ~~measured data~~ electropherogram using data analysis, and
 - determining the quality value, which indicates the extent of degradation of the ~~biomolecule~~ RNA sample, from the extracted features using a quality algorithm,
- wherein the quality algorithm has been derived from:
- collecting a statistically significant number of trial ~~measured data~~ electropherograms covering a prescribed set of ~~biomolecule~~ RNA samples,
 - assigning a quality label, which indicates the extent that the trial ~~measured data~~ electropherogram exhibits signs of degradation, to every trial ~~measured data~~ electropherogram,

extracting features from the trial ~~measured data~~ electropherograms using data analysis,

determining functional interrelations among the quality labels and one or more combinations of the extracted features,

assigning a rating factor to every functional interrelation and

specifying the functional interrelation that has the highest rating factor as the quality algorithm, when run on a data processing system such as a computer.

26. (currently amended) An apparatus for determining the extent of degradation, expressed in terms of a quality value, of a ~~biomolecule~~ an RNA sample, based on ~~measured data~~ an electropherogram of the ~~biomolecule~~ RNA sample, the apparatus comprising: a processing unit adapted for extracting a number of prescribed features from the ~~measured data~~ electropherogram using data analysis, and for determining the quality value, which indicates the extent of degradation of the ~~biomolecule~~ RNA sample, from the extracted features using a quality algorithm, wherein the quality algorithm has been derived from:

collecting a statistically significant number of trial ~~measured data~~ electropherograms covering a prescribed set of ~~biomolecule~~ RNA samples,

assigning a quality label, which indicates the extent that the trial ~~measured data~~ electropherogram exhibits signs of degradation, to every trial ~~measured data~~ electropherogram,

extracting features from the trial ~~measured data~~ electropherograms using data analysis,

determining functional interrelations among the quality labels and one or more combinations of the extracted features,

assigning a rating factor to every functional interrelation and

specifying the functional interrelation that has the highest rating factor as the quality algorithm, when run on a data processing system such as a computer.

27. (canceled)

28. (previously presented) A method for determining the extent of degradation, expressed in terms of a quality value, of an RNA sample, the method comprising:

separating the RNA sample by mobility, using an electrophoresis device, to generate an electropherogram,

extracting a number of prescribed features from the electropherogram using data analysis, and

determining the quality value, which indicates the extent of degradation of the RNA sample, from the extracted features using a quality algorithm,

wherein the quality algorithm has been derived by mathematical modeling from a statistically significant number of trial RNA electropherograms covering a prescribed set of RNA samples.

29. (previously presented) A method for determining the extent of degradation, expressed in terms of a quality value, of an RNA sample, the method comprising:

separating the RNA sample by mobility, using an electrophoresis device, to generate an electropherogram,

subdividing the electropherogram into segments comprising an 18S-region, a 28S-region, and at least one region selected from the group consisting of a prerregion, a marker region, a 5S-region, a fast region, an interregion, and a postregion,

extracting a number of prescribed features from the electropherogram using data analysis, wherein at least some of the prescribed features are extracted from the segments of the electropherogram, and

determining the quality value, which indicates the extent of degradation of the RNA sample, from the extracted features using a quality algorithm.

30. (currently amended) A method for determining the extent of degradation, expressed in terms of a quality value, of ~~a biomolecule~~ an RNA sample, the method comprising:

separating the ~~biomolecule~~ RNA sample by ~~one or more molecular characteristics~~ mobility, using an electrophoresis device, to generate ~~measured data~~ an electropherogram,

extracting a number of prescribed features from the ~~measured data~~ electropherogram using data analysis, and

determining the quality value, which indicates the extent of degradation of the ~~biomolecule~~ RNA sample, from the extracted features using a quality algorithm.

31. (canceled)

32. (currently amended) The method of claim ~~31~~ 30, wherein the electropherogram is subdivided into segments to extract features therefrom.

33. (previously presented) The method of claim 32, wherein the segments comprise a fast region, an 18S-region, and a 28S-region.

34. (previously presented) The method of claim 33, wherein the electropherogram can be represented as a data curve or a smoothed data curve and wherein one or more of the following prescribed features from the segments of the data curve, or the smoothed data curve, of the electropherogram are determined in the data analysis of the electropherogram:

the maximum and minimum value occurring within the segment,

the slope and y-intercept of the interpolating straight line fitted to the points on the curve falling within the bounds of the segment,

the y-values of this interpolating straight line at the start and end points of the segment,

the area under the curve,

the area under the interpolating straight line, the ratios of the latter areas to the area under the entire data curve,

the deviation of the interpolating straight line from the data curve, or

the deviations of the original and smoothed data curve from one another.